

SEQUENCE LISTING

<110> Wright, Susan C.
Larrick, James W.
Nock, Steffen R.
Wilson, David S.

<120> Cell-Killing Molecules and Methods of Use Thereof

<130> ABSALUS-08602

<160> 81

<170> PatentIn version 3.2

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<211> 314

<212> PRT

<213> Sus scrofa

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Asp Ile Ala His Thr Pro Gly Val Ala Ala Asp Leu Ser His Ile Glu
35 40 45

Thr Arg Ala Thr Val Lys Gly Tyr Leu Gly Pro Glu Gln Leu Pro Asp
50 55 60

Cys Leu Lys Gly Cys Asp Val Val Val Ile Pro Ala Gly Val Pro Arg
65 70 75 80

Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn Thr Asn Ala Thr Ile
85 90 95

Val Ala Thr Leu Thr Ala Ala Cys Ala Gln His Cys Pro Asp Ala Met
100 105 110

Ile Cys Ile Ile Ser Asn Pro Val Asn Ser Thr Ile Pro Ile Thr Ala
115 120 125

Glu Val Phe Lys Lys His Gly Val Tyr Asn Pro Asn Lys Ile Phe Gly
130 135 140

Val Thr Thr Leu Asp Ile Val Arg Ala Asn Ala Phe Val Ala Glu Leu
145 150 155 160

Lys Gly Leu Asp Pro Ala Arg Val Ser Val Pro Val Ile Gly Gly His
165 170 175

Ala Gly Lys Thr Ile Ile Pro Leu Ile Ser Gln Cys Thr Pro Lys Val
180 185 190

Asp Phe Pro Gln Asp Gln Leu Ser Thr Leu Thr Gly Arg Ile Gln Glu
195 200 205

Ala Gly Thr Glu Val Val Lys Ala Lys Ala Gly Ala Gly Ser Ala Thr
210 215 220

Leu Ser Met Ala Tyr Ala Gly Ala Arg Phe Val Phe Ser Leu Val Asp
225 230 235 240

Ala Met Asn Gly Lys Glu Gly Val Val Glu Cys Ser Phe Val Lys Ser
245 250 255

Gln Glu Thr Asp Cys Pro Tyr Phe Ser Thr Pro Leu Leu Leu Gly Lys
260 265 270

Lys Gly Ile Glu Lys Asn Leu Gly Ile Gly Lys Ile Ser Pro Phe Glu
275 280 285

Glu Lys Met Ile Ala Glu Ala Ile Pro Glu Leu Lys Ala Ser Ile Lys
290 295 300

Lys Gly Glu Glu Phe Val Lys Asn Met Lys
305 310

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Gly Ala Arg Phe Val Phe Ser Leu Val Asp Ala Met Asn Gly Lys Glu
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Gly Val Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Asp Cys Pro
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Tyr Phe Ser Thr Pro Leu Leu Leu Gly Lys Lys Gly Ile Glu Lys Asn
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Leu Gly Ile Gly Lys Ile Ser Pro
65 70

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<213> Sus scrofa

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Gly Ala Arg Phe Val Phe Ser Leu Val Asp Ala Met Asn Gly Lys Glu
20 25 30

Gly Val Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Asp Cys Pro
35 40 45

Tyr Phe Ser Thr Pro Leu Leu Leu Gly Lys Lys Gly Ile Glu Lys Asn
50 55 60

Leu Gly Ile Gly Lys Ile Ser Pro Phe Glu Glu Lys Met Ile Ala Glu
65 70 75 80

Ala Ile Pro Glu Leu Lys Ala Ser Ile Lys Lys Gly Glu Glu Phe Val
85 90 95

Lys Asn Met Lys
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Ser Gly Gly Ile Gly Gln Pro Leu Ser Leu Leu Lys Asn Ser Pro
35 40 45

Leu Val Ser Arg Leu Thr Leu Tyr Asp Ile Ala His Thr Pro Gly Val
50 55 60

Ala Ala Asp Leu Ser His Ile Glu Thr Lys Ala Ala Val Lys Gly Tyr
65 70 75 80

Leu Gly Pro Glu Gln Leu Pro Asp Cys Leu Lys Gly Cys Asp Val Val
85 90 95

Val Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp
100 105 110

Leu Phe Asn Thr Asn Ala Thr Ile Val Ala Thr Leu Thr Ala Ala Cys
115 120 125

Ala Gln His Cys Pro Glu Ala Met Ile Cys Val Ile Ala Asn Pro Val
130 135 140

Asn Ser Thr Ile Pro Ile Thr Ala Glu Val Phe Lys Lys His Gly Val
145 150 155 160

Tyr Asn Pro Asn Lys Ile Phe Gly Val Thr Thr Leu Asp Ile Val Arg
165 170 175

Ala Asn Thr Phe Val Ala Glu Leu Lys Gly Leu Asp Pro Ala Arg Val
180 185 190

Asn Val Pro Val Ile Gly Gly His Ala Gly Lys Thr Ile Ile Pro Leu
195 200 205

Ile Ser Gln Cys Thr Pro Lys Val Asp Phe Pro Gln Asp Gln Leu Thr
210 215 220

Ala Leu Thr Gly Arg Ile Gln Glu Ala Gly Thr Glu Val Val Lys Ala
225 230 235 240

Lys Ala Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly Ala
245 250 255

Arg Phe Val Phe Ser Leu Val Asp Ala Met Asn Gly Lys Glu Gly Val
260 265 270

Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Glu Cys Thr Tyr Phe
275 280 285

Ser Thr Pro Leu Leu Leu Gly Lys Lys Gly Ile Glu Lys Asn Leu Gly
290 295 300

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305 310 315 320

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325 330 335

Leu Lys

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<213> Homo sapiens

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Gly Ala Arg Phe Val Phe Ser Leu Val Asp Ala Met Asn Gly Lys Glu
20 25 30

Gly Val Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Glu Cys Thr
35 40 45

Tyr Phe Ser Thr Pro Leu Leu Leu Gly Lys Lys Gly Ile Glu Lys Asn
50 55 60

Leu Gly Ile Gly Lys Val Ser Ser
65 70

<210> 7
<211> 100
<212> PRT
<213> Homo sapiens

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Lys Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala
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Gly Ala Arg Phe Val Phe Ser Leu Val Asp Ala Met Asn Gly Lys Glu
20 25 30

Gly Val Val Glu Cys Ser Phe Val Lys Ser Gln Glu Thr Glu Cys Thr
35 40 45

Tyr Phe Ser Thr Pro Leu Leu Leu Gly Lys Lys Gly Ile Glu Lys Asn
50 55 60

Leu Gly Ile Gly Lys Val Ser Ser Phe Glu Glu Lys Met Ile Ser Asp
65 70 75 80

Ala Ile Pro Glu Leu Lys Ala Ser Ile Lys Lys Gly Glu Asp Phe Val
85 90 95

Lys Thr Leu Lys
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1 5 10 15

Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
20 25 30

Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
35 40 45

Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
50 55 60

Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
65 70 75 80

Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
85 90 95

Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
100 105 110

Ala Gly Gly Ala Val Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro
115 120 125

Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg
130 135 140

Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
145 150 155 160

Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
165 170 175

Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
180 185 190

Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
195 200 205

Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
210 215 220

Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Phe Gly Asn
225 230 235 240

Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn
245 250 255

Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg
260 265 270

Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly
275 280 285

Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu
290 295 300

Ser Pro Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly
305 310 315 320

Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr
325 330 335

Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr
340 345 350

Leu Tyr Val Thr Pro Glu Val Thr Glu
355 360

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gaatga						1086

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 20 25 30

Arg Leu Pro Gly Asn Leu Phe Gln Arg Trp His Val Pro Leu Glu Leu
 35 40 45

Gln Met Thr Arg Gln Met Ala Ser Ser Gly Ala Ser Gly Gly Lys Ile
 50 55 60

Asp Asn Ser Val Leu Val Ile Val Gly Leu Ser Thr Val Gly Ala
 65 70 75 80

Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn
 85 90 95

Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys
 100 105 110

Ala Ala Leu Ser Ala Ser Glu Gly Glu Glu Val Pro Gln Asp Lys Ala
 115 120 125

Pro Ser His Val Pro Phe Leu Leu Ile Gly Gly Thr Ala Ala Phe
 130 135 140

Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu
145 150 155 160

Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser
165 170 175

Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Leu Arg
180 185 190

Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro
195 200 205

Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly
210 215 220

Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Asp
225 230 235 240

Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys
245 250 255

Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg
260 265 270

Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly
275 280 285

Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr
290 295 300

Ile Ile Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly
305 310 315 320

Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu
325 330 335

Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr
340 345 350

Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile
355 360 365

Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys
370 375 380

Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu
385 390 395 400

Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser
405 410 415

Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn
420 425 430

Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly
435 440 445

Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu
450 455 460

Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser
465 470 475 480

Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly
485 490 495

Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr
500 505 510

Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile
515 520 525

Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Glu Ile Thr Ile Pro
530 535 540

Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr
545 550 555 560

Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile
565 570 575

Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile Ala Arg Lys Ile Ile
580 585 590

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595 600 605

Asn Ile His Glu Asp
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Ser Thr Phe Leu Ser Gln Thr Thr Tyr Ala Leu Ile Glu Ala Ile Thr			
35	40	45	
Glu Tyr Thr Lys Ala Val Tyr Thr Leu Thr Ser Leu Tyr Arg Gln Tyr			
50	55	60	
Thr Ser Leu Leu Gly Lys Met Asn Ser Glu Glu Glu Asp Glu Val Trp			
65	70	75	80
Gln Val Ile Ile Gly Ala Arg Ala Glu Met Thr Ser Lys His Gln Glu			
85	90	95	
Tyr Leu Lys Leu Glu Thr Thr Trp Met Thr Ala Val Gly Leu Ser Glu			
100	105	110	
Met Ala Ala Glu Ala Ala Tyr Gln Thr Gly Ala Asp Gln Ala Ser Ile			
115	120	125	
Thr Ala Arg Asn His Ile Gln Leu Val Lys Leu Gln Val Glu Glu Val			
130	135	140	
His Gln Leu Ser Arg Lys Ala Glu Thr Lys Leu Ala Glu Ala Gln Ile			
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Glu Glu Leu Arg Gln Lys Thr Gln Glu Glu Gly Glu Glu Arg Ala Glu			
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Ser Glu Gln Glu Ala Tyr Leu Arg Glu Asp			
180	185		

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 gtggaagagg tgcaccagct ctcccgaaa gcagaaacca agctggcaga agcacagata 480
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 gcctacctgc gtgaggattg a 561

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 <212> PRT
 <213> Homo sapiens

<400> 14

Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
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 20 25 30

Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
 35 40 45

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
 50 55 60

Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
 65 70 75 80

Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
 85 90 95

Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
 100 105 110

His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115 120 125

Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130 135 140

Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145 150 155 160

Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165 170 175

Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
180 185 190

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195 200 205

Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
245 250 255

Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
260 265 270

Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
275 280 285

Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
290 295 300

Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
305 310 315 320

Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
325 330 335

Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
340 345 350

Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
355 360 365

Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly
370 375 380

Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
385 390 395 400

Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
405 410 415

Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
420 425 430

Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
435 440 445

Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
450 455 460

Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
465 470 475 480

Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
485 490 495

Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
500 505 510

Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
515 520 525

Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
530 535 540

Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
545 550 555 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
580 585 590

Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
 610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
 625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
 645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
 660 665 670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
 675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
 690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys
 705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
 725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
 740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
 755 760 765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
 770 775 780

<210> 15
 <211> 2349
 <212> DNA
 <213> Homo sapiens

<400> 15
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 caggggcggg tgcccggaggc gcggcccaac agcatggtgg tggAACACCC cgagttcctc 180
 aaggcaggga aggaggctgg cctgcagatc tggcgtgtgg agaagttcga tctggtgccc 240
 gtgccccacca acctttatgg agacttcttc acggggcgcacg cctacgtcat cctgaagaca 300
 gtgcagctga ggaacggaaa tctgcagtat gacctccact actggctggg caatgagtgc 360

agccaggatg	agagcggggc	ggccgccc	tttaccgtgc	agctggatga	ctac	ctgaac	420											
ggccggggccg	tgcagcac	ccg	tgaggtccag	ggcttc	gagt	cggccac	480											
ttcaagtctg	gcctgaagta	caagaa	agga	ggtgtggc	at	caggattcaa	540											
cccaacgagg	tggtggtgca	gagact	cttc	caggtcaa	ag	ggcggcgtgt	600											
accgaggtac	ctgtgtcctg	ggagag	cttc	aacaatggcg	actg	cattcat	660											
ggcaacaaca	tccaccagt	gtgtgg	ttcc	aacagcaatc	ggtatgaa	actgaagg	720											
acacaggtgt	ccaagggcat	ccggg	acaac	gagcggag	tg	gccgggccc	780											
tctgaggagg	gcactgag	cc	gaggc	gat	gat	gtgcac	840											
cctgcaggta	ccgaggac	ac	cgcc	aggag	at	gcggcc	900											
tacaagg	tct	caatgg	tg	aggaccat	tccgt	tccc	960											
ttcgcccagg	gggc	ccctg	aa	gtcagagg	tgctt	catcc	tggtg	ctga	tgaga	accccc	1020							
aaaatctt	tg	tctg	gaa	agg	caagc	agg	aac	acgg	agg	ag	tgcc	ctcaaa	1080					
acagc	cct	c	ctg	actt	cat	ca	ca	agatgg	ac	actc	aggt	ctcggt	cctt	1140				
cctgagggcg	gtgagac	cc	actgtt	caag	cagtt	ttca	aga	actgg	cg	ggacc	cagac	gg	1200					
cagacagat	gc	ctgg	ggtt	ttt	gtc	ctt	tcc	agcc	ata	tcg	ccaa	gt	ggcgggt	1260				
cccttcgac	ccg	cc	ccct	gc	acac	ctcc	act	gccat	gg	cc	cag	ca	ggat	1320				
gacgatgg	ca	ggc	ccag	aa	acag	atct	gg	aga	atcg	aa	gttcca	ac	aa	gg	1380			
gacc	cct	gcca	catatgg	aca	tt	catatg	g	ggc	gac	ag	act	ttt	ct	gtaca	actac	1440		
cgccatgg	g	cc	gccc	agg	g	cata	ttt	gc	ata	tc	act	gg	cc	gt	ctt	acc	1500	
gatgagg	tcg	ctg	cat	c	tc	c	tc	tc	act	gg	at	gagg	at	cc	t	acc	tg	1560
cctgtcc	aga	g	cc	gt	gt	gg	tt	cc	aa	gg	ttt	gg	tt	gg	tt	gg	tt	1620
ggga	agg	cc	ca	tg	cc	aa	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1680
gccagc	ac	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1740
gtattgc	cta	agg	gg	cc	ac	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1800
gccgc	c	ctt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1860
ctg	ctc	agg	gg	gg	cc	aa	cc	ct	gt	cc	cc	cc	cc	cc	cc	cc	cc	1920
ttctgg	agg	cc	ctt	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	1980
aagatgg	at	cc	at	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2040
atc	gaag	agg	tt	c	c	c	c	c	c	c	c	c	c	c	c	c	c	2100
ctgg	ac	cc	ct	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	2160
acaga	ac	cc	ct	tc	ta	agc	gg	ta	ac	g	ac	gg	cc	aa	tc	gg	at	2220

eggacgccccca tcaccgtggt gaagcaaggc tttgagccctc cctcctttgt gggctgggccc 2280
 cttggctggg atgatgatta ctggtctgtg gaccgccttg acagggccat ggctgagctg 2340
 gctgcctga 2349

<210> 16
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45

Phe Ser Ser Gln Pro Gly His Thr Pro His Thr Ala Ala Ser Arg Asp
 50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
 85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
 100 105 110

Ala Glu Met Ser Arg Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
195 200 205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
210 215 220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
225 230 235

<210> 17
<211> 720
<212> DNA
<213> Homo sapiens

<400> 17
atggcgacg ctgggagaac agggtacgat aaccgggaga tagtgatgaa gtacatccat 60
tataagctgt cgcaaggggg ctacgagtgg gatgcgggag atgtgggcgc cgcccccgg 120
ggggccgccc cgcgcgggg catcttctcc tcgcagcccg ggcacacgccc ccatacagcc 180
gcacccgggg acccggtcgc caggacctcg ccgcgtcaga ccccggtgc ccccggtgc 240
gccgcggggc ctgcgtctcag cccgggtgcca cctgtggtcc acctgaccct cgcaggcc 300
ggcgacgact tctcccgccg ctaccgcgc gacttcgcg agatgtccag gcagctgcac 360
ctgacgcctc tcaccgcgcg gggacgctt gccacgggtgg tggaggagct cttcaggac 420
ggggtaact gggggaggat tgtggccttc tttgagttcg gtggggatcat gtgtgtggag 480
agcgtaacc gggagatgtc gcccctggtg gacaacatcg ccctgtggat gactgagtac 540
ctgaaccggc acctgcacac ctggatccag gataacggag gctgggatgc ctttggaa 600
ctgtacggcc ccagcatgcg gcctctgttt gatttctctt ggctgtctct gaagactctg 660
ctcagttgg ccctgggtgg agcttgcatt accctgggtg cctatctggg ccacaagtga 720

<210> 18
<211> 164
<212> PRT
<213> Homo sapiens

<400> 18

Met Asp Gly Ser Gly Glu Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser
1 5 10 15

Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln
20 25 30

Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
35 40 45

Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
50 55 60

Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
65 70 75 80

Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
85 90 95

Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
100 105 110

Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Gly Val Lys Trp
115 120 125

Arg Asp Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Arg Phe
130 135 140

Thr Cys Leu Ser Ile Pro Arg Ser Trp Asp Tyr Arg Pro Cys Ala Pro
145 150 155 160

Arg Cys Arg Asn

<210> 19
<211> 495
<212> DNA
<213> Homo sapiens

<400> 19
atggacgggt ccggggagca gcccagaggc ggggggcccc caagctctga gcagatcatg 60
aagacagggg ccctttgct tcagggttc atccaggatc gagcagggcg aatggggggg 120
gaggcacccg agctggccct ggacccggtg cctcaggatg cgtccaccaa gaagctgagc 180
gagtgtctca agcgcacatcg ggacgaactg gacagtaaca tggagctgca gaggatgatt 240
gccgcgtgg acacagactc ccccccggagag gtcttttcc gagtggcagc tgacatgttt 300
tctgacggca acttcaactg gggccgggtt gtcgccttt tctactttgc cagcaaactg 360
gtgctcaagg ctggcgtgaa atggcgtgat ctgggctcac tgcaacctct gcctcctggg 420
ttcaagcgat tcacctgcct cagcatccca aggagctggg attacaggcc ctgtgcacca 480
aggtgcccggaa actga 495

<210> 20
<211> 168
<212> PRT
<213> Homo sapiens

<400> 20

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
1 5 10 15

Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
20 25 30

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
35 40 45

Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
50 55 60

Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
65 70 75 80

Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
85 90 95

Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
100 105 110

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
115 120 125

Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
130 135 140

Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
145 150 155 160

Arg Gly Ser Ser Ala Pro Ser Gln
165

<210> 21
<211> 507
<212> DNA
<213> Homo sapiens

<400> 21

atgttccaga tccccagagtt tgagccgagt gagcaggaag actccagctc tgcagagagg 60

ggcctgggcc ccagccccgc aggggacggg ccctcaggct ccggcaagca tcatcgccag 120

gccccaggcc tcctgtggga cgccagtcac cagcaggagc agccaaccag cagcagccat 180

catggaggcg	ctggggctgt	ggagatccgg	agtccacaca	gctcctaccc	cgcggggacg	240
gaggacgacg	aaggatggg	ggaggagccc	agcccttgc	ggggccgctc	gcgctcggcg	300
cccccaacc	tctgggcagc	acagcgctat	ggccgcgagc	tccggaggat	gagtgacgag	360
tttgtggact	ccttaagaa	gggacttcct	cgcccgaaaga	gcccggcac	agcaacgcag	420
atgcggcaaa	gctccagctg	gacgcgagtc	ttccagtcct	ggtggatcg	gaacttggc	480
agggaaagct	ccgccccctc	ccagtga				507

<210> 22
 <211> 241
 <212> PRT
 <213> Homo sapiens
 <400> 22

Met Cys Ser Gly Ala Gly Val Met Met Ala Arg Trp Ala Ala Arg Gly
 1 5 10 15

Arg Ala Gly Trp Arg Ser Thr Val Arg Ile Leu Ser Pro Leu Gly His
 20 25 30

Cys Glu Pro Gly Val Ser Arg Ser Cys Arg Ala Ala Gln Ala Met Asp
 35 40 45

Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile Thr Asn
 50 55 60

Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser Phe Arg
 65 70 75 80

Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala Pro Gln
 85 90 95

Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser Ser His
 100 105 110

Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu Asp Ile
 115 120 125

Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp
 130 135 140

Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln Leu Arg
 145 150 155 160

Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala Thr Ala
 165 170 175

Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys Glu Lys
180 185 190

Thr Met Leu Val Leu Ala Leu Leu Ala Lys Lys Val Ala Ser His
195 200 205

Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn Phe Ile
210 215 220

Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn Gly Met
225 230 235 240

Asp

<210> 23
<211> 726
<212> DNA
<213> Homo sapiens

<400> 23
atgtgcagcg gtgctgggtt catgtggct cgggtggcag cgaggggcccgg ggcgggctgg 60
aggagcacag tgcggattct gtcgcccactg ggacactgtg aaccaggagt gagtcggagc 120
tgccgcgctg cccaggccat ggactgtgag gtcaacaacg gttccagcct cagggatgag 180
tgcatcacaa acctactggt gttggcttc ctccaaagct gttctgacaa cagttccgc 240
agagagctgg acgcactggg ccacgagctg ccagtgctgg ctccccagtg ggagggctac 300
gatgagctgc agactgtatgg caacccgcagc agccactccc gcttggaaag aatagaggca 360
gattctgaaa gtcaagaaga catcatccgg aatattgcca ggcacccctcgcc ccaggtcg 420
gacagcatgg accgttagcat ccctccggc ctggtaacg gcctggccct gcagctcagg 480
aacaccagcc ggtcggagga ggaccggaaac agggacctgg ccactgcctt ggagcagctg 540
ctgcaggcct acccttagaga catggagaag gagaagacca tgctggtgctt ggccctgctg 600
ctggccaaga aggtggccag tcacacgccc tccttgctcc gtgatgtctt tcacacaaca 660
gtgaatttta ttaaccagaa cctacgcacc tacgtgagga gcttagccag aaatgggatg 720
gactga 726

<210> 24
<211> 297
<212> PRT
<213> Homo sapiens

<400> 24

Met Arg Ala Leu Arg Ala Gly Leu Thr Leu Ala Ser Gly Ala Gly Leu
1 5 10 15

Gly Ala Val Val Glu Gly Trp Arg Arg Arg Arg Glu Asp Ala Arg Ala
20 25 30

Ala Leu Gly Leu Leu Gly Arg Leu Pro Val Leu Pro Val Ala Ala Ala
35 40 45

Ala Glu Leu Pro Pro Val Pro Gly Gly Pro Arg Gly Pro Gly Glu Leu
50 55 60

Ala Lys Tyr Gly Leu Pro Gly Leu Ala Gln Leu Lys Ser Arg Glu Ser
65 70 75 80

Tyr Val Leu Cys Tyr Asp Pro Arg Thr Arg Gly Ala Leu Trp Val Val
85 90 95

Glu Gln Leu Arg Pro Glu Arg Leu Arg Gly Asp Gly Asp Arg Arg Glu
100 105 110

Cys Asp Phe Arg Glu Asp Asp Ser Val His Ala Tyr His Arg Ala Thr
115 120 125

Asn Ala Asp Tyr Arg Gly Ser Gly Phe Asp Arg Gly His Leu Ala Ala
130 135 140

Ala Ala Asn His Arg Trp Ser Gln Lys Ala Met Asp Asp Thr Phe Tyr
145 150 155 160

Leu Ser Lys Val Ala Pro Gln Val Pro His Leu Asn Gln Asn Ala Trp
165 170 175

Asn Asn Leu Glu Lys Tyr Ser Arg Ser Leu Thr Arg Ser Tyr Gln Asn
180 185 190

Val Tyr Val Cys Thr Gly Pro Leu Phe Leu Pro Arg Thr Glu Ala Asp
195 200 205

Gly Lys Ser Tyr Val Lys Tyr Gln Val Ile Gly Lys Asn His Val Ala
210 215 220

Val Pro Thr His Phe Phe Lys Val Leu Ile Leu Glu Ala Ala Gly Gly
225 230 235 240

Gln Ile Glu Leu Arg Thr Tyr Val Met Pro Asn Ala Pro Val Asp Glu
245 250 255

Ala Ile Pro Leu Glu Arg Phe Leu Val Pro Ile Glu Ser Ile Glu Arg
260 265 270

Ala Ser Gly Leu Leu Phe Val Pro Asn Ile Leu Ala Arg Ala Gly Ser
275 280 285

Leu Lys Ala Ile Thr Ala Gly Ser Lys
290 295

<210> 25
<211> 894
<212> DNA
<213> Homo sapiens

<400> 25
atgcgggcccgc tgccggccgg cctgaccctg gctgcggccgc cggggctggg tgccggtcgtc 60
gagggctggc ggccggcggccg ggaggacgcgc cggccggccgc tggactgct gggccggctg 120
ccctgtctgc ccgtggccggc ggcagccgag ttgccccctg tgcccgaaaa accccggcc 180
ccggccgagt tggccaagta cgggctgccc gggctggccgc agctcaagag ccgcgagtcg 240
tacgtgctgt gctacgaccc gcgcacccgc ggcgcgtct gggtggtgg acaactgcga 300
cccgagcgtc tccgcggcga cggcgaccgg cgccgactgct acttccgcga ggacgactcg 360
gtgcacgcgt accaccgtgc caccaacgccc gactaccgcg gcagtggctt cgaccgcgtt 420
cacctggccg ccgcgcggccaa ccaccgctgg agccagaagg ccatggacga cacgttctac 480
ctgagcaaag tgcgcggccaa ggtgcggccac ctcaaccaga atgcctggaa caacctggag 540
aaatatagcc gcagcttgac ccgcagctac caaaacgtct atgtctgcac agggccactc 600
ttcctgccccca ggacagagggc tggatggaaa tcctacgtaa agtaccaggt catcgccaa 660
aaccacgtgg cagtgcggccac acacttcttc aaggtgctga tcctggagggc agcaggtggg 720
caaattgagc tccgcaccta cgtgatgccc aacgcacctg tggatggggc catcccaactg 780
gagcgcttcc tggtgcccat cgagagcatt gagcgggctt cggggctgct ctttgc 840
aacatcctgg cgccggcagg cagcctcaag gccatcacgg cgggcagtaa gtga 894

<210> 26
<211> 338
<212> PRT
<213> Homo sapiens

<400> 26

Met Leu Gln Lys Pro Lys Ser Val Lys Leu Arg Ala Leu Arg Ser Pro
1 5 10 15

Arg Lys Phe Gly Val Ala Gly Arg Ser Cys Gln Glu Val Leu Arg Lys
20 25 30

Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu
35 40 45

Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro
50 55 60

Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
65 70 75 80

Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
85 90 95

Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
100 105 110

Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
115 120 125

Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
130 135 140

Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys
145 150 155 160

Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
165 170 175

Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser
180 185 190

Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
195 200 205

Arg Gly Ala Lys Gly Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe
210 215 220

Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser
225 230 235 240

Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp
245 250 255

Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
260 265 270

Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
275 280 285

Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
290 295 300

Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
305 310 315 320

Ile Tyr Lys Pro Gln Thr Arg Leu Lys Arg Lys Gln Pro Val Arg Lys
325 330 335

Arg Gln

<210> 27
<211> 1017
<212> DNA
<213> Homo sapiens

<400> 27
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gtggctggcc ggagctgcc a ggaggtgctg cgcaagggt gtctccgctt ccagctccct 120
gagcgcgggtt cccggctgtg cctgtacgag gatggcacgg agctgacgga agattactc 180
cccaagtgttc ccgacaacgc cgagctggtg ctgctcacct tggccagggc ctggcagggc 240
tatgtgagcg acatcaggcg cttcctcagt gcatttcacg agccacaggt ggggctcatac 300
caggccgccc agcagctgct gtgtgatgag caggccccac agaggcagag gctgctggct 360
gacctcctgc acaacgtcag ccagaacatc gcccggcaga cccgggctga ggaccggccg 420
tggtttgaag gcttggagtc ccgatttcag agcaagtctg gctatctgag atacagctgt 480
gagagccgga tccggagtt a cctgagggag gtgagctcct acccctccac ggtgggtgcg 540
gaggctcagg aggaatttcgc ggggtcctc ggctccatgt gccagaggct ccggtccatg 600
cagtacaatg gca gactactt cgacagagga gccaaggcg gca gcccgcct ctgcacaccg 660
gaaggctggt tctcctgcc a ggtcccttt gacatggaca gctgcttatac aagacactcc 720

atcaaccct acagtaacag ggagagcagg atcctttca gcacctggaa cctggatcac	780
ataatagaaa agaaacgcac catcattctt acactggtgg aagcaattaa ggaacaagat	840
ggaagagaag tggactggga gtatTTTat ggcctgctt ttacctcaga gaacctaaaa	900
ctagtgcaca ttgtctgccs taagaaaacc acccacaagg tcaactgtga cccaaaggaga	960
atctacaaac cccagacaag gttgaagcgg aagcagcctg tgccggaaacg ccagtga	1017

<210> 28
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Glu Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg			
1	5	10	15

Thr Leu Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His		
20	25	30

Gly Val Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp		
35	40	45

Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala		
50	55	60

Glu Asp Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro			
65	70	75	80

Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr		
85	90	95

Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp		
100	105	110

Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala		
115	120	125

Arg Gln Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu		
130	135	140

Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu			
145	150	155	160

Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln		
165	170	175

Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
180 185 190

Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
195 200 205

Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
210 215 220

Thr Gly Ile Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
225 230 235 240

Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
245 250 255

Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala
260 265 270

Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
275 280 285

Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
290 295 300

Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
305 310 315 320

Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr
325 330

<210> 29
<211> 996
<212> DNA
<213> Homo sapiens

<400> 29
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ctatcagagg aggacctcca gatgcttgtt gacgctccct gctcagacct ggctcaggaa 480

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aaagagggca	gcctcttgtc	aaagcagggaa	gagtccaaag	ctgccttgg	tgaggaggtg	660
gatcagtag	acacgggtat	cagcagagag	acccctcgg	acgttgcgt	ggcgagccac	720
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aagacggaga	ctgttcagga	ggcctgtgag	cgggagctcg	ccctgcgcct	gcagcagacg	900
cagagcttc	attctctccg	gagcatctca	gcaagcaagg	cctcaccacc	tggtgacctg	960
cagaatccta	agegagccag	acaggatccc	acatag			996

<210> 30
 <211> 1207
 <212> PRT
 <213> Homo sapiens
 <400> 30

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Phe Val Ser Leu Ser Ala Pro Gln His Trp Ser Cys Pro Glu Gly Thr
 20 25 30

Leu Ala Gly Asn Gly Asn Ser Thr Cys Val Gly Pro Ala Pro Phe Leu
 35 40 45

Ile Phe Ser His Gly Asn Ser Ile Phe Arg Ile Asp Thr Glu Gly Thr
 50 55 60

Asn Tyr Glu Gln Leu Val Val Asp Ala Gly Val Ser Val Ile Met Asp
 65 70 75 80

Phe His Tyr Asn Glu Lys Arg Ile Tyr Trp Val Asp Leu Glu Arg Gln
 85 90 95

Leu Leu Gln Arg Val Phe Leu Asn Gly Ser Arg Gln Glu Arg Val Cys
 100 105 110

Asn Ile Glu Lys Asn Val Ser Gly Met Ala Ile Asn Trp Ile Asn Glu
 115 120 125

Glu Val Ile Trp Ser Asn Gln Gln Glu Gly Ile Ile Thr Val Thr Asp
 130 135 140

Met Lys Gly Asn Asn Ser His Ile Leu Leu Ser Ala Leu Lys Tyr Pro
145 150 155 160

Ala Asn Val Ala Val Asp Pro Val Glu Arg Phe Ile Phe Trp Ser Ser
165 170 175

Glu Val Ala Gly Ser Leu Tyr Arg Ala Asp Leu Asp Gly Val Gly Val
180 185 190

Lys Ala Leu Leu Glu Thr Ser Glu Lys Ile Thr Ala Val Ser Leu Asp
195 200 205

Val Leu Asp Lys Arg Leu Phe Trp Ile Gln Tyr Asn Arg Glu Gly Ser
210 215 220

Asn Ser Leu Ile Cys Ser Cys Asp Tyr Asp Gly Gly Ser Val His Ile
225 230 235 240

Ser Lys His Pro Thr Gln His Asn Leu Phe Ala Met Ser Leu Phe Gly
245 250 255

Asp Arg Ile Phe Tyr Ser Thr Trp Lys Met Lys Thr Ile Trp Ile Ala
260 265 270

Asn Lys His Thr Gly Lys Asp Met Val Arg Ile Asn Leu His Ser Ser
275 280 285

Phe Val Pro Leu Gly Glu Leu Lys Val Val His Pro Leu Ala Gln Pro
290 295 300

Lys Ala Glu Asp Asp Thr Trp Glu Pro Glu Gln Lys Leu Cys Lys Leu
305 310 315 320

Arg Lys Gly Asn Cys Ser Ser Thr Val Cys Gly Gln Asp Leu Gln Ser
325 330 335

His Leu Cys Met Cys Ala Glu Gly Tyr Ala Leu Ser Arg Asp Arg Lys
340 345 350

Tyr Cys Glu Asp Val Asn Glu Cys Ala Phe Trp Asn His Gly Cys Thr
355 360 365

Leu Gly Cys Lys Asn Thr Pro Gly Ser Tyr Tyr Cys Thr Cys Pro Val
370 375 380

Gly Phe Val Leu Leu Pro Asp Gly Lys Arg Cys His Gln Leu Val Ser
385 390 395 400

Cys Pro Arg Asn Val Ser Glu Cys Ser His Asp Cys Val Leu Thr Ser
405 410 415

Glu Gly Pro Leu Cys Phe Cys Pro Glu Gly Ser Val Leu Glu Arg Asp
420 425 430

Gly Lys Thr Cys Ser Gly Cys Ser Ser Pro Asp Asn Gly Gly Cys Ser
435 440 445

Gln Leu Cys Val Pro Leu Ser Pro Val Ser Trp Glu Cys Asp Cys Phe
450 455 460

Pro Gly Tyr Asp Leu Gln Leu Asp Glu Lys Ser Cys Ala Ala Ser Gly
465 470 475 480

Pro Gln Pro Phe Leu Leu Phe Ala Asn Ser Gln Asp Ile Arg His Met
485 490 495

His Phe Asp Gly Thr Asp Tyr Gly Thr Leu Leu Ser Gln Gln Met Gly
500 505 510

Met Val Tyr Ala Leu Asp His Asp Pro Val Glu Asn Lys Ile Tyr Phe
515 520 525

Ala His Thr Ala Leu Lys Trp Ile Glu Arg Ala Asn Met Asp Gly Ser
530 535 540

Gln Arg Glu Arg Leu Ile Glu Glu Gly Val Asp Val Pro Glu Gly Leu
545 550 555 560

Ala Val Asp Trp Ile Gly Arg Arg Phe Tyr Trp Thr Asp Arg Gly Lys
565 570 575

Ser Leu Ile Gly Arg Ser Asp Leu Asn Gly Lys Arg Ser Lys Ile Ile
580 585 590

Thr Lys Glu Asn Ile Ser Gln Pro Arg Gly Ile Ala Val His Pro Met
595 600 605

Ala Lys Arg Leu Phe Trp Thr Asp Thr Gly Ile Asn Pro Arg Ile Glu
610 615 620

Ser Ser Ser Leu Gln Gly Leu Gly Arg Leu Val Ile Ala Ser Ser Asp
625 630 635 640

Leu Ile Trp Pro Ser Gly Ile Thr Ile Asp Phe Leu Thr Asp Lys Leu
645 650 655

Tyr Trp Cys Asp Ala Lys Gln Ser Val Ile Glu Met Ala Asn Leu Asp
660 665 670

Gly Ser Lys Arg Arg Arg Leu Thr Gln Asn Asp Val Gly His Pro Phe
675 680 685

Ala Val Ala Val Phe Glu Asp Tyr Val Trp Phe Ser Asp Trp Ala Met
690 695 700

Pro Ser Val Ile Arg Val Asn Lys Arg Thr Gly Lys Asp Arg Val Arg
705 710 715 720

Leu Gln Gly Ser Met Leu Lys Pro Ser Ser Leu Val Val Val His Pro
725 730 735

Leu Ala Lys Pro Gly Ala Asp Pro Cys Leu Tyr Gln Asn Gly Gly Cys
740 745 750

Glu His Ile Cys Lys Lys Arg Leu Gly Thr Ala Trp Cys Ser Cys Arg
755 760 765

Glu Gly Phe Met Lys Ala Ser Asp Gly Lys Thr Cys Leu Ala Leu Asp
770 775 780

Gly His Gln Leu Leu Ala Gly Gly Glu Val Asp Leu Lys Asn Gln Val
785 790 795 800

Thr Pro Leu Asp Ile Leu Ser Lys Thr Arg Val Ser Glu Asp Asn Ile
805 810 815

Thr Glu Ser Gln His Met Leu Val Ala Glu Ile Met Val Ser Asp Gln
820 825 830

Asp Asp Cys Ala Pro Val Gly Cys Ser Met Tyr Ala Arg Cys Ile Ser
835 840 845

Glu Gly Glu Asp Ala Thr Cys Gln Cys Leu Lys Gly Phe Ala Gly Asp
850 855 860

Gly Lys Leu Cys Ser Asp Ile Asp Glu Cys Glu Met Gly Val Pro Val
865 870 875 880

Cys Pro Pro Ala Ser Ser Lys Cys Ile Asn Thr Glu Gly Gly Tyr Val
885 890 895

Cys Arg Cys Ser Glu Gly Tyr Gln Gly Asp Gly Ile His Cys Leu Asp
900 905 910

Ile Asp Glu Cys Gln Leu Gly Val His Ser Cys Gly Glu Asn Ala Ser
915 920 925

Cys Thr Asn Thr Glu Gly Gly Tyr Thr Cys Met Cys Ala Gly Arg Leu
930 935 940

Ser Glu Pro Gly Leu Ile Cys Pro Asp Ser Thr Pro Pro Pro His Leu
945 950 955 960

Arg Glu Asp Asp His His Tyr Ser Val Arg Asn Ser Asp Ser Glu Cys
965 970 975

Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr
980 985 990

Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile
995 1000 1005

Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
1010 1015 1020

His Ala Gly His Gly Gln Gln Gln Lys Val Ile Val Val Ala Val
1025 1030 1035

Cys Val Val Val Leu Val Met Leu Leu Leu Leu Ser Leu Trp Gly
1040 1045 1050

Ala His Tyr Tyr Arg Thr Gln Lys Leu Leu Ser Lys Asn Pro Lys
1055 1060 1065

Asn Pro Tyr Glu Glu Ser Ser Arg Asp Val Arg Ser Arg Arg Pro
1070 1075 1080

Ala Asp Thr Glu Asp Gly Met Ser Ser Cys Pro Gln Pro Trp Phe
1085 1090 1095

Val Val Ile Lys Glu His Gln Asp Leu Lys Asn Gly Gly Gln Pro
1100 1105 1110

Val Ala Gly Glu Asp Gly Gln Ala Ala Asp Gly Ser Met Gln Pro
1115 1120 1125

Thr Ser Trp Arg Gln Glu Pro Gln Leu Cys Gly Met Gly Thr Glu
1130 1135 1140

Gln Gly Cys Trp Ile Pro Val Ser Ser Asp Lys Gly Ser Cys Pro
1145 1150 1155

Gln Val Met Glu Arg Ser Phe His Met Pro Ser Tyr Gly Thr Gln
1160 1165 1170

Thr Leu Glu Gly Gly Val Glu Lys Pro His Ser Leu Leu Ser Ala
1175 1180 1185

Asn Pro Leu Trp Gln Gln Arg Ala Leu Asp Pro Pro His Gln Met
1190 1195 1200

Glu Leu Thr Gln
1205

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<211> 3624
<212> DNA
<213> Homo sapiens

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tgtgtgggtc ctgcaccctt cttaatttc tcccatggaa atagtatctt taggattgac 120
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acagtaacag atatgaaagg aaataattcc cacattctt taagtgcatt aaaatatcct 420
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720

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<210> 32
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 32

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
180 185 190

<210> 33
<211> 576
<212> DNA
<213> Homo sapiens

<400> 33
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gaacgtactt gcagatgtga caagccgagg cggtga 576

<210> 34
<211> 175
<212> PRT
<213> Homo sapiens

<400> 34

Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1 5 10 15

Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
20 25 30

Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
35 40 45

Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
50 55 60

Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65 70 75 80

Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
85 90 95

Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
100 105 110

Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
115 120 125

Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130 135 140

Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145 150 155 160

Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
165 170 175

<210> 35
<211> 528
<212> DNA
<213> Homo sapiens

<400> 35

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tctacttccc tgagtccctt ctaccttcgg ccaccctcct tcctgcgggc acccagctgg 180

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catggaaaac	atgaagagcg	ccaggatgaa	catggttca	tctccaggga	gttccacagg	360
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ggggtcctca	ctgtgaatgg	accaaggaaa	caggtctctg	gccctgagcg	caccattccc	480
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<210> 36
 <211> 378
 <212> PRT
 <213> *Drosophila melanogaster*
 <400> 36

Met Thr Met Ser Thr Asn Asn Cys Glu Ser Met Thr Ser Tyr Phe Thr
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Asn Ser Tyr Met Gly Ala Asp Met His His Gly His Tyr Pro Gly Asn
 20 25 30

Gly Val Thr Asp Leu Asp Ala Gln Gln Met His His Tyr Ser Gln Asn
 35 40 45

Ala Asn His Gln Gly Asn Met Pro Tyr Pro Arg Phe Pro Pro Tyr Asp
 50 55 60

Arg Met Pro Tyr Tyr Asn Gly Gln Gly Met Asp Gln Gln Gln Gln His
 65 70 75 80

Gln Val Tyr Ser Arg Pro Asp Ser Pro Ser Ser Gln Val Gly Gly Val
 85 90 95

Met Pro Gln Ala Gln Thr Asn Gly Gln Leu Gly Val Pro Gln Gln Gln
 100 105 110

Gln Gln Gln Gln Gln Pro Ser Gln Asn Gln Gln Gln Gln Ala
 115 120 125

Gln Gln Ala Pro Gln Gln Leu Gln Gln Leu Pro Gln Val Thr Gln
 130 135 140

Gln Val Thr His Pro Gln Gln Gln Gln Pro Val Val Tyr Ala
 145 150 155 160

Ser Cys Lys Leu Gln Ala Ala Val Gly Gly Leu Gly Met Val Pro Glu
 165 170 175

Gly Gly Ser Pro Pro Leu Val Asp Gln Met Ser Gly His His Met Asn
180 185 190

Ala Gln Met Thr Leu Pro His His Met Gly His Pro Gln Ala Gln Leu
195 200 205

Gly Tyr Thr Asp Val Gly Val Pro Asp Val Thr Glu Val His Gln Asn
210 215 220

His His Asn Met Gly Met Tyr Gln Gln Ser Gly Val Pro Pro Val
225 230 235 240

Gly Ala Pro Pro Gln Gly Met Met His Gln Gly Gln Gly Pro Pro Gln
245 250 255

Met His Gln Gly His Pro Gly Gln His Thr Pro Pro Ser Gln Asn Pro
260 265 270

Asn Ser Gln Ser Ser Gly Met Pro Ser Pro Leu Tyr Pro Trp Met Arg
275 280 285

Ser Gln Phe Gly Lys Cys Gln Glu Arg Lys Arg Gly Arg Gln Thr Tyr
290 295 300

Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His Phe Asn Arg
305 310 315 320

Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala Leu Cys Leu
325 330 335

Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp
340 345 350

Lys Lys Glu Asn Lys Thr Lys Gly Glu Pro Gly Ser Gly Gly Glu Gly
355 360 365

Asp Glu Ile Thr Pro Pro Asn Ser Pro Gln
370 375

<210> 37
 <211> 1137
 <212> DNA
 <213> Drosophila melanogaster

<400> 37
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<210> 38
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly
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Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly
 20 25 30

Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly
 35 40 45

Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys
50 55 60

Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His
65 70 75 80

Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys
85 90 95

Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
100 105 110

Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn
115 120 125

Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys
130 135 140

Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp
145 150 155 160

Ser Arg Glu

<210> 39
<211> 492
<212> DNA
<213> Homo sapiens

<400> 39
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tgggaccgtc agggagaaaa tggccagatg atgagctgca catgtcttgg gaacggaaaa 180
ggagaattca agtgtgaccc tcatgaggca acgtgttatg atgatggaa gacataccac 240
gtaggagaac agtggcagaa ggaatatctc ggtgccattt gctcctgcac atgctttgga 300
ggccagcggg gctggcgctg tgacaactgc cgcagacctg ggggtgaacc cagtcccgaa 360
ggcactactg gccagtctta caaccagtat tctcagagat accatcagag aacaaacact 420
aatgttaatt gccaattga gtgtttcatg cctttagatg tacaggctga cagagaagat 480
tcccgagagt ag 492

<210> 40
<211> 282
<212> PRT
<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
275 280

<210> 41
<211> 849
<212> DNA
<213> Homo sapiens

<400> 41
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gccaccctcg tcagctacat tgcgcagatc ctgagccgct atgacatcgc cctggtccag 180
gaggtcagag acagccacct gactgccgtg gggaaagctgc tggacaacct caatcaggat 240
gcaccagaca cctatcacta cgtggtcagt gagccactgg gacggAACAG ctataaggag 300
cgctacctgt tcgtgtacag gcctgaccag gtgtctgcgg tggacagcta ctactacgt 360
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ttctcccggt tcacagaggt cagggagttt gccattgttc ccctgcattgc ggccccgggg 480
gacgcagtag ccgagatcga cgctctctat gacgtctacc tggatgtcca agagaaatgg 540
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tcccagtggcgtt catccatccg cctgtggaca agccccacct tccagtggtt gatccccgac 660
agcgctgaca ccacagctac acccacgcac tgtgcctatg acaggatcgt ggttgcagg 720
atgctgctcc gaggcgccgt tggatccgac tcggctcttc cctttaactt ccaggtgcc 780
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ctgaagtga 849

<210> 42
<211> 360
<212> PRT
<213> Homo sapiens

<400> 42

Met Ile Pro Leu Leu Leu Ala Ala Leu Leu Cys Val Pro Ala Gly Ala
1 5 10 15

Leu Thr Cys Tyr Gly Asp Ser Gly Gln Pro Val Asp Trp Phe Val Val
20 25 30

Tyr Lys Leu Pro Ala Leu Arg Gly Ser Gly Glu Ala Ala Gln Arg Gly
35 40 45

Leu Gln Tyr Lys Tyr Leu Asp Glu Ser Ser Gly Gly Trp Arg Asp Gly
50 55 60

Arg Ala Leu Ile Asn Ser Pro Glu Gly Ala Val Gly Arg Ser Leu Gln
65 70 75 80

Pro Leu Tyr Arg Ser Asn Thr Ser Gln Leu Ala Phe Leu Leu Tyr Asn
85 90 95

Asp Gln Pro Pro Gln Pro Ser Lys Ala Gln Asp Ser Ser Met Arg Gly
100 105 110

His Thr Lys Gly Val Leu Leu Asp His Asp Gly Gly Phe Trp Leu
115 120 125

Val His Ser Val Pro Asn Phe Pro Pro Pro Ala Ser Ser Ala Ala Tyr
130 135 140

Ser Trp Pro His Ser Ala Cys Thr Tyr Gly Gln Thr Leu Leu Cys Val
145 150 155 160

Ser Phe Pro Phe Ala Gln Phe Ser Lys Met Gly Lys Gln Leu Thr Tyr
165 170 175

Thr Tyr Pro Trp Val Tyr Asn Tyr Gln Leu Glu Gly Ile Phe Ala Gln
180 185 190

Glu Phe Pro Asp Leu Glu Asn Val Val Lys Gly His His Val Ser Gln
195 200 205

Glu Pro Trp Asn Ser Ser Ile Thr Leu Thr Ser Gln Ala Gly Ala Val
210 215 220

Phe Gln Ser Phe Ala Lys Phe Ser Lys Phe Gly Asp Asp Leu Tyr Ser
 225 230 235 240

 Gly Trp Leu Ala Ala Ala Leu Gly Thr Asn Leu Gln Val Gln Phe Trp
 245 250 255

 His Lys Thr Val Gly Ile Leu Pro Ser Asn Cys Ser Asp Ile Trp Gln
 260 265 270

 Val Leu Asn Val Asn Gln Ile Ala Phe Pro Gly Pro Ala Gly Pro Ser
 275 280 285

 Phe Asn Ser Thr Glu Asp His Ser Lys Trp Cys Val Ser Pro Lys Gly
 290 295 300

 Pro Trp Thr Cys Val Gly Asp Met Asn Arg Asn Gln Gly Glu Glu Gln
 305 310 315 320

 Arg Gly Gly Thr Leu Cys Ala Gln Leu Pro Ala Leu Trp Lys Ala
 325 330 335

 Phe Gln Pro Leu Val Lys Asn Tyr Gln Pro Cys Asn Gly Met Ala Arg
 340 345 350

 Lys Pro Ser Arg Ala Tyr Lys Ile
 355 360

 <210> 43
 <211> 1083
 <212> DNA
 <213> Homo sapiens

 <400> 43
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 tggcgggacg gcagggcact catcaacagc ccggaggggg ccgtggcccg aagcctgcag 240
 ccgctgtacc ggagcaacac cagccagctc gccttcctgc tctacaatga ccaaccgcct 300
 caacccagca aggctcagga ctcttccatg cgtggcaca cgaagggtgt cctgctcctt 360
 gaccacgatg ggggcttctg gctggtccac agtgtaccta acttccctcc accggcctcc 420
 tctgctgcat acagctggcc tcatagcgcc tgtacctacg ggcagaccct gctctgtgtg 480
 tctttccct tcgctcagtt ctcgaagatg ggcaagcagc tgacctacac ctacccctgg 540
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gteaagggec accacgttag ccaagaaccc tggaaacagea geataeacact cacatccccag	660
gecggggctg tttccagag ctttgc当地 ttcagcaat ttggagatga cctgtactcc	720
ggctgggtgg cagcagccct tggtaccaac ctgcaggtcc agttctggca caaaactgta	780
ggcatcctgc cctctaactg ctcggatatc tggcaggtte tgaatgtgaa ccagatagct	840
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tcccaaaag ggccctggac ctgcgtgggt gacatgaatc ggaaccagg agaggagcaa	960
cgggggtgggg gcacactgtg tgcccagctg ccagccctct ggaaagcctt ccagccgctg	1020
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taa	1083

<210> 44
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 44

Met Asp Asn Ala Arg Met Asn Ser Phe Leu Glu Tyr Pro Ile Leu Ser			
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10	15		

Ser Gly Asp Ser Gly Thr Cys Ser Ala Arg Ala Tyr Pro Ser Asp His			
20	25	30	
30			

Arg Ile Thr Thr Phe Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly			
35	40	45	
45			

Gly Asp Asp Arg Phe Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro			
50	55	60	
60			

His His His His His His His His His Pro Gln Pro Ala Thr Tyr			
65	70	75	80
75	80		

Gln Thr Ser Gly Asn Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly			
85	90	95	
95			

Pro Ser Tyr Gly Ser Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala			
100	105	110	
110			

Leu Asn Gln Glu Ala Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro			
115	120	125	
125			

Ala Val Tyr Ser Gly Asn Leu Ser Ser Pro Met Val Gln His His His			
130	135	140	
140			

His His Gln Gly Tyr Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile
145 150 155 160

His His Ser Tyr Gly Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr
165 170 175

Asn Asn Ser Leu Ser Pro Leu His Ala Ser His Gln Glu Ala Cys Arg
180 185 190

Ser Pro Ala Ser Glu Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met
195 200 205

Lys Val Lys Arg Asn Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly
210 215 220 225

Tyr Leu Gly Gln Pro Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln
225 230 235 240

Leu Thr Glu Leu Glu Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg
245 250 255

Ala Arg Arg Val Glu Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln
260 265 270

Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu
275 280 285

Lys Glu Gly Leu Leu Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp
290 295 300

Glu Lys Ala Glu Glu Ser Ser Glu Lys Ser Ser Ser Pro Cys Val
305 310 315 320

Pro Ser Pro Gly Ser Ser Thr Ser Asp Thr Leu Thr Thr Ser His
325 330 335

<210> 45

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 45

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gcggtcagcg ccaacagttg cggcgccgac gaccgcttcc tagtggcag ggggtgcag 180

atcggttcgc cccaccacca ccaccaccac caccatcacc acccccagcc ggctacctac 240

cagacttccg ggaacctggg ggtgtcctac tcccactcaa gttgtggtcc aagctatggc	300
tcacagaact tcagtgcgcc ttacagcccc tacgcgttaa atcaggaagc agacgtaagt	360
ggtgggtacc cccagtgcgc tcccgtgtt tactctggaa atctctcatc tcccatggtc	420
cagcatcacc accaccacca gggttatgct gggggcgccgg tgggctcgcc tcaatacatt	480
caccactcat atggacagga gcaccagagc ctggccctgg ctacgtataa taactccttg	540
tcccctctcc acgccagcca ccaagaagcc tgcgtctccc cgcgcacggg gacatcttct	600
ccagcgcaga ctttgactg gatgaaagtc aaaagaaacc ctcccaaaac agggaaagtt	660
ggagagtacg gctacctggg tcaacccaac gcgggtgcga ccaacttcac taccaagcag	720
ctcacggaac tggagaagga gttccacttc aacaagtacc tgacgcgcgc ccgcagggtg	780
gagatcgctg catccctgca gctcaacgag acccaagtga agatctgggtt ccagaaccgc	840
cgaatgaagc aaaagaaacg tgagaaggag ggtctttgc ccatctctcc ggccaccccg	900
ccaggaaacg acgagaaggc cgaggaatcc tcagagaagt coagctttc gccctgcgtt	960
ccttccccgg ggtcttctac ctcagacact ctgactacct cccactga	1008

<210> 46
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
 1 5 10 15

Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
 20 25 30

Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
 35 40 45

Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
 50 55 60

Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
 65 70 75 80

Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
 85 90 95

Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
 100 105 110

Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125

Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
130 135 140 145

Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
145 150 155 160

Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
165 170 175

Ser Asn Arg Lys
180

<210> 47
<211> 543
<212> DNA
<213> Homo sapiens

<400> 47
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tgctgcattg ctgcttacccg ccccaagttag accctgtgcg gcggggagct ggtggacacc
ctccagttcg tctgtgggaa ccgcggcttc tacttcagca ggcccgcaag ccgtgtgagc 120
cgtcgcagcc gtggcatcgt tgaggagtgc tggttccgca gctgtgaccc ggcctccctg
gagacgtact gtgctacccc cgccaagtcc gagagggacg tgcgacccc tccgaccgtg 180
cttccggaca acttccccag atacccctgt ggcaagttct tccaatatga cacctggaaag
cagtccaccc agcgccctgcg cagggggctg cctgcctcc tgcgtgcccc ccggggtcac 240
gtgctcgcca aggagctcga ggcgttcagg gaggccaaac gtcaccgtcc cctgattgct
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tga 360
543

<210> 48
<211> 59
<212> PRT
<213> Homo sapiens

<400> 48

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
1 5 10 15

Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
20 25 30

Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
35 40 45

Thr Arg Asp Arg Ser Asp Gln His Asn Thr Lys
50 55

<210> 49
<211> 180
<212> DNA
<213> Homo sapiens

<400> 49
atggctgaag gggaaatcac cacccacaca gcccgtaccg agaagtttaa tctgcctcca 60
gggaattaca agaagcccaa actcctctac tgttagcaacg ggggcccactt cctgaggatc 120
cttccggatg gcacagtggc tgggacaagg gacaggagcg accagcacaa caccaaatga 180

<210> 50
<211> 102
<212> PRT
<213> Human immunodeficiency virus

<400> 50

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Asn His Pro Gly Ser
1 5 10 15

Gln Pro Gln Thr Pro Cys Asn Lys Cys Tyr Cys Lys His Cys Ser Tyr
20 25 30

His Cys Leu Val Cys Phe Gln Thr Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Ser Thr Pro Pro Ser Ser Glu Ser
50 55 60

His Gln Asn Pro Leu Ser Lys Gln Pro Leu Pro Gln Thr Arg Gly Asp
65 70 75 80

Gln Thr Gly Ser Glu Glu Gln Lys Lys Lys Val Glu Ser Lys Thr Glu
85 90 95

Thr Asp Pro Tyr Asp Trp
100

<210> 51		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 51		
gaattcgcag atctgagcca catcgagacc		30
<210> 52		
<211> 37		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 52		
gtcgactcag accacctccg tgccggcctc ctggatc		37
<210> 53		
<211> 32		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 53		
gaattcaagg ctaaagccgg agcaggtct gc		32
<210> 54		
<211> 36		
<212> DNA		
<213> Artificial Sequence		
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<223> Synthetic		
<400> 54		
gtcgactcac ttcagggtct tcacgaaatc ttcccc		36
<210> 55		
<211> 36		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic		
<400> 55		
ggccgaattc aaggctaaag ccggagcagg ctctgc		36

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<210> 56
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
aatttgcgac ttatttttt catttcatgc ggegggtctg aaacccaaatt ttaatctggc 60
gettcagggt cttcacgaaa tcttcccc 88

<210> 57
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 58
<211> 36
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 58

Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1 5 10 15

Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
20 25 30

Leu Ser Lys Gln
35

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Cys
1 5 10

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<210> 60
<211> 17
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 60

Thr Arg Gln Ala Arg Arg Asn Arg Arg Arg Arg Trp Arg Glu Arg Gln
1 5 10 15

Arg

<210> 61
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61

Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
1 5 10 15

Lys Lys Arg Lys Val
20

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 63
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63

Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

<210> 64
<211> 12
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 64

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro
1 5 10

<210> 65
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 65

Pro Leu Leu Lys Lys Ile Lys Gln
1 5

<210> 66
<211> 8
<212> PRT
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<400> 66

Pro Pro Gln Lys Lys Ile Lys Ser
1 5

<210> 67
<211> 7
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<400> 67

Pro Gln Pro Lys Lys Lys Pro
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 68

Ser Lys Arg Val Ala Lys Arg Lys Leu
1 5

<210> 69
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69

Gly Arg Arg Arg Arg
1 5

<210> 70
<211> 155
<212> PRT
<213> Homo sapiens

<400> 70

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
1 5 10 15

Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
20 25 30

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
35 40 45

Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
50 55 60

Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65 70 75 80

Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
85 90 95

Val Thr Asp Glu Cys Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
100 105 110

Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
115 120 125

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
130 135 140

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145 150 155

<210> 71
<211> 6757
<212> DNA
<213> Homo sapiens

<400> 71
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ggtgccagat tagcggacgg ctgcccgcgg ttgcaacggg atccccggcg ctgcagctt 180
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ggggccgtgcc ccggagcggg tcggaggccg gggccggggc cgggggacgg cggctcccc 420
cgctggctcca gctggctcggt gatccggcc gggcccccgc gggaccatgg cagccggag 480
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cttcaaggac cccaaagcggc tgtactgcaa aaacgggggc ttcttcctgc gcatccaccc 600
cgacggccga gttgacgggg tccggagaa gagcgcaccct cacatcaagc tacaacttca 660
agcagaagag agaggagttg tgtctatcaa aggagtgtgt gctaaccgtt acctggctat 720
gaaggaagat ggaagattac tggcttctaa atgtgttacg gatgagtgtt tctttttga 780
acgattggaa tctaataact acaataactta ccggtaagg aaatacacca gttggtatgt 840
ggcactgaaa cgaactgggc agtataaact tggatccaaa acaggacctg ggcagaaagc 900
tatactttt cttccaatgt ctgcttaagag ctgattttaa tggccacatc taatctcatt 960
tcacatgaaa gaagaagtat atttttagaaa tttgttaatg agagtaaaag aaaataaaatg 1020
tgtatagctc agtttggata attggtaaaa caattttta tccagtagta aaatatgtaa 1080
ccattgtccc agtaaagaaa aataacaaaa gttgtaaaat gtatattctc ctttttatat 1140
tgcatctgct gttaccctgtt gaaaccttacc tagagcaatg atcttttca cgcatttgct 1200
ttattcgaaa agaggctttt aaaatgtgca tggtagaaa caaaatttct tcatggaaat 1260
catatacatt agaaaatcactc agtcagatgt ttaatcaatc caaaatgtcc actatttctt 1320

atgtcatatgg ttagtctaca tgtttctaaa catataaaatg tgaatttaat caattccttt	1380
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aactgctgga agttcttcca cagtcaggc aattttgtca aacccttctc tgtacccata	1500
cagcagcagc ctagcaactc tgctggat gggagttgtat tttcagtct tcgcccaggc	1560
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gtgctgtgc cgaataactca ggacggaccc gaattctgtat ttataccag tctcttcaaa	1740
aacttctcga accgctgtgt ctccctacgta aaaaaagaga tgtacaatc aataataatt	1800
acacttttag aaactgtatc atcaaagatt ttcaatggaa gtagcattat gtaaaggctc	1860
aaaacattac cctaacaag taaagtttc aatacaatt ctgtccttg tggatataaa	1920
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gcatggctgc agttcctttg ttcttgaga taagattcca aagaacttag attcatttct	2160
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tttcatca	aaaatatgct	attnaaat	ctatcccta	tattgtat	ctaattcagat	6660
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<210> 72
<211> 513
<212> PRT
<213> Homo sapiens

<400> 72

Met Phe Ala Asp Arg Trp Leu Phe Ser Thr Asn His Lys Asp Ile Gly
1 5 10 15

Thr Leu Tyr Leu Leu Phe Gly Ala Trp Ala Gly Val Leu Gly Thr Ala
20 25 30

Leu Ser Leu Leu Ile Arg Ala Glu Leu Gly Gln Pro Gly Asn Leu Leu
35 40 45

Gly Asn Asp His Ile Tyr Asn Val Ile Val Thr Ala His Ala Phe Val
50 55 60

Met Ile Phe Phe Met Val Met Pro Ile Met Ile Gly Gly Phe Gly Asn
65 70 75 80

Trp Leu Val Pro Leu Met Ile Gly Ala Pro Asp Met Ala Phe Pro Arg
85 90 95

Met Asn Asn Met Ser Phe Trp Leu Leu Pro Pro Ser Leu Leu Leu
100 105 110

Leu Ala Ser Ala Met Val Glu Ala Gly Ala Gly Thr Gly Trp Thr Val
115 120 125

Tyr Pro Pro Leu Ala Gly Asn Tyr Ser His Pro Gly Ala Ser Val Asp
130 135 140

Leu Thr Ile Phe Ser Leu His Leu Ala Gly Val Ser Ser Ile Leu Gly
145 150 155 160

Ala Ile Asn Phe Ile Thr Thr Ile Ile Asn Met Lys Pro Pro Ala Met
165 170 175

Thr Gln Tyr Gln Thr Pro Leu Phe Val Trp Ser Val Leu Ile Thr Ala
180 185 190

Val Leu Leu Leu Ser Leu Pro Val Leu Ala Ala Gly Ile Thr Met
195 200 205

Leu Leu Thr Asp Arg Asn Leu Asn Thr Thr Phe Phe Asp Pro Ala Gly
210 215 220

Gly Gly Asp Pro Ile Leu Tyr Gln His Leu Phe Trp Phe Phe Gly His
225 230 235 240

Pro Glu Val Tyr Ile Leu Ile Leu Pro Gly Phe Gly Met Ile Ser His
245 250 255

Ile Val Thr Tyr Tyr Ser Gly Lys Lys Glu Pro Phe Gly Tyr Met Gly
260 265 270

Met Val Trp Ala Met Met Ser Ile Gly Phe Leu Gly Phe Ile Val Trp
275 280 285

Ala His His Met Phe Thr Val Gly Met Asp Val Asp Thr Arg Ala Tyr
290 295 300

Phe Thr Ser Ala Thr Met Ile Ile Ala Ile Pro Thr Gly Val Lys Val
305 310 315 320

Phe Ser Trp Leu Ala Thr Leu His Gly Ser Asn Met Lys Trp Ser Ala
325 330 335

Ala Val Leu Trp Ala Leu Gly Phe Ile Phe Leu Phe Thr Val Gly Gly
340 345 350

Leu Thr Gly Ile Val Leu Ala Asn Ser Ser Leu Asp Ile Val Leu His
355 360 365

Asp Thr Tyr Tyr Val Val Ala His Phe His Tyr Val Leu Ser Met Gly
370 375 380

Ala Val Phe Ala Ile Met Gly Gly Phe Ile His Trp Phe Pro Leu Phe
385 390 395 400

Ser Gly Tyr Thr Leu Asp Gln Thr Tyr Ala Lys Ile His Phe Thr Ile
405 410 415

Met Phe Ile Gly Val Asn Leu Thr Phe Phe Pro Gln His Phe Leu Gly
420 425 430

Leu Ser Gly Met Pro Arg Arg Tyr Ser Asp Tyr Pro Asp Ala Tyr Thr
435 440 445

Thr Trp Asn Ile Leu Ser Ser Val Gly Ser Phe Ile Ser Leu Thr Ala
450 455 460

Val Met Leu Met Ile Phe Met Ile Trp Glu Ala Phe Ala Ser Lys Arg
465 470 475 480

Lys Val Leu Met Val Glu Glu Pro Ser Met Asn Leu Glu Trp Leu Tyr
485 490 495

Gly Cys Pro Pro Pro Tyr His Thr Phe Glu Glu Pro Val Tyr Met Lys
500 505 510

Ser

<210> 73
<211> 1542
<212> DNA
<213> Homo sapiens

<400> 73
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ttattcggcg catgagctgg agtcctaggc acagctctaa gcctccttat tcgagccgag 120
ctgggccagc caggcaacct tctaggtaac gaccacatct acaacgttat cgtcacagcc 180
catgcatttg taataatctt cttcatagta atacccatca taatcgagg ctttggcaac 240
tgactagttc ccctaataat cggtgcccc gatatggcgt ttcccccgt aaacaacata 300
agcttctgac tcttacctcc ctctctccta ctccctgctcg catctgctat agtggaggcc 360
ggagcaggaa caggttgaac agtctaccct cccttagcag ggaactactc ccaccctgga 420
gcctccgtag acctaaccat cttctccta cacctagcag gtgtctcctc tatcttaggg 480
gccatcaatt tcatcacaac aattatcaat ataaaacccc ctgccataac ccaataccaa 540
acgccccctct tcgtctgatc cgtcctatac acagcagtcc tacttctcct atctctccca 600
gtcctagctg ctggcatcac tatactacta acagaccgca acctcaacac caccttctc 660
gaccccgccg gaggaggaga ccccattcta taccaacacc tattctgatt tttcggtcac 720
cctgaagttt atattcttat cctaccaggo ttccgaaataa tctcccatat tgtaacttac 780
tactccggaa aaaaagaacc atttggatac ataggtatgg tctgagctat gatataatt 840
ggcttcttag ggtttatcgt gtgagcacac catataattta cagtaggaat agacgttagac 900
acacgagcat atttcacctc cgctaccata atcatcgcta tccccaccgg cgtcaaagta 960
tttagctgac tcgccacact ccacggaagc aatatgaaat gatctgctgc agtgcctga 1020
gccttaggat tcatcttct tttcaccgta ggtggcctga ctggcattgt attagcaaac 1080
tcatcactag acatcgtaact acacgacacg tactacgttg tagctcactt ccactatgtc 1140
ctatcaatag gagctgtatt tgccatcata ggaggcttca ttcaactgatt tccccattc 1200
tcaggctaca ccctagacca aacctacgcc aaaatccatt tcactatcat attcatggc 1260
gtaaatctaa ctttcttccc acaacacttt ctggcctat ccggaatgcc ccgacgttac 1320

tcggactace ccgatgcata eaccaeatga aacatctat catctgtagg ctcattcatt 1380
tctctaacag cagtaatatt aataatttc atgatttgag aagccttcgc ttcgaagcga 1440
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ccctaccaca cattcgaaga acccgatac ataaaatcta ga 1542

<210> 74
<211> 219
<212> PRT
<213> Homo sapiens

<400> 74

Met Ser Ser His Leu Val Glu Pro Pro Pro Pro Leu His Asn Asn Asn
1 5 10 15

Asn Asn Cys Glu Glu Asn Glu Gln Ser Leu Pro Pro Pro Ala Gly Leu
20 25 30

Asn Ser Ser Trp Val Glu Leu Pro Met Asn Ser Ser Asn Gly Asn Asp
35 40 45

Asn Gly Asn Gly Lys Asn Gly Gly Leu Glu His Val Pro Ser Ser Ser
50 55 60

Ser Ile His Asn Gly Asp Met Glu Lys Ile Leu Leu Asp Ala Gln His
65 70 75 80

Glu Ser Gly Gln Ser Ser Ser Arg Gly Ser Ser His Cys Asp Ser Pro
85 90 95

Ser Pro Gln Glu Asp Gly Gln Ile Met Phe Asp Val Glu Met His Thr
100 105 110

Ser Arg Asp His Ser Ser Gln Ser Glu Glu Glu Val Val Glu Gly Glu
115 120 125

Lys Glu Val Glu Ala Leu Lys Lys Ser Ala Asp Trp Val Ser Asp Trp
130 135 140

Ser Ser Arg Pro Glu Asn Ile Pro Pro Lys Glu Phe His Phe Arg His
145 150 155 160

Pro Lys Arg Ser Val Ser Leu Ser Met Arg Lys Ser Gly Ala Met Lys
165 170 175

Lys Gly Gly Ile Phe Ser Ala Glu Phe Leu Lys Val Phe Ile Pro Ser
180 185 190

Leu Phe Leu Ser His Val Leu Ala Leu Gly Leu Gly Ile Tyr Ile Gly
195 200 205

Lys Arg Leu Ser Thr Pro Ser Ala Ser Thr Tyr
210 215

<210> 75
<211> 660
<212> DNA
<213> Homo sapiens

<400> 75
atgttgtccc acctagtcg a cccggccg cccctgcaca acaacaacaa caactgcgag 60
gaaaatgagc agtctctgcc cccggccggcc ggcctaaca gttcctgggt ggagctaccc 120
atgaacagca gcaatggcaa tgataatggc aatggggaaa atggggggct ggaacacgta 180
ccatcctcat cctccatcca caatggagac atggagaaga ttcttttggg tgcacaacat 240
gaatcaggac agagtagttc cagaggeagt tctcaetgtg acagcccttc gccacaagaa 300
gatgggcaga tcatgtttga tgtggaaatg cacaaccagca gggaccatag ctetcaagtca 360
gaagaagaag ttgtagaagg agagaaggaa gtcgagggtt tgaagaaaag tgcggactgg 420
gtatcaact ggtccagtag aeccgaaaac attccaccca aggagttcca cttcagacac 480
cctaaacgtt ctgtgtcttt aagcatgagg aaaagtggag ccatgaagaa agggggattt 540
ttctccgcag aatttctgaa ggtgttcatt ccatctctct tcctttctca tgttttggct 600
ttggggctag gcatctatat tggaaagcga ctgagcacac cctctgccag cacctactga 660

<210> 76
<211> 194
<212> PRT
<213> Homo sapiens

<400> 76

Met Ser Gln Asn Gly Ala Pro Gly Met Gln Glu Glu Ser Leu Gln Gly
1 5 10 15

Ser Trp Val Glu Leu His Phe Ser Asn Asn Gly Asn Gly Gly Ser Val
20 25 30

Pro Ala Ser Val Ser Ile Tyr Asn Gly Asp Met Glu Lys Ile Leu Leu
35 40 45

Asp Ala Gln His Glu Ser Gly Arg Ser Ser Ser Lys Ser Ser His Cys
50 55 60

Asp Ser Pro Pro Arg Ser Gln Thr Pro Gln Asp Thr Asn Arg Ala Ser
65 70 75 80

Glu Thr Asp Thr His Ser Ile Gly Glu Lys Asn Ser Ser Gln Ser Glu
85 90 95

Glu Asp Asp Ile Glu Arg Arg Lys Glu Val Glu Ser Ile Leu Lys Lys
100 105 110

Asn Ser Asp Trp Ile Trp Asp Trp Ser Ser Arg Pro Glu Asn Ile Pro
115 120 125

Pro Lys Glu Phe Leu Phe Lys His Pro Lys Arg Thr Ala Thr Leu Ser
130 135 140

Met Arg Asn Thr Ser Val Met Lys Lys Gly Gly Ile Phe Ser Ala Glu
145 150 155 160

Phe Leu Lys Val Phe Leu Pro Ser Leu Leu Ser His Leu Leu Ala
165 170 175

Ile Gly Leu Gly Ile Tyr Ile Gly Arg Arg Leu Thr Thr Ser Thr Ser
180 185 190

Thr Phe

<210> 77
<211> 585
<212> DNA
<213> Homo sapiens

<400> 77
atgtcgcaga acggagcgcc cgggatgcag gaggagagcc tgcagggctc ctgggttagaa 60
ctgcacttca gcaataatgg gaacgggggc agcgttccag cctcggttcc tatttataat 120
ggagacatgg aaaaaatact gctggacgca cagcatgagt ctggacggag tagctccaag 180
agctctcaact gtgacagccc acctcgctcg cagacaccac aagataccaa caggcattct 240
gaaacagata cccatagcat tggagagaaa aacagctcac agtctgagga agatgatatt 300
gaaagaagga aagaagtta aagcatctt aagaaaaact cagattggat atgggattgg 360
tcaagtcggc cggaaaatat tccccccaag gagttcctct ttaaacaccc gaagcgcacg 420
gccaccctca gcatgaggaa cacgagcgtc atgaagaaag ggggcattt ctctgcagaa 480
tttctgaaag ttttccttcc atctctgctg ctctctcatt tgcggccat cggattgggg 540
atctatattg gaaggcgtct gacaacctcc accagcacct tttga 585

<210> 78
<211> 219
<212> PRT
<213> Homo sapiens

<400> 78

Met Glu Tyr Leu Ser Ala Leu Asn Pro Ser Asp Leu Leu Arg Ser Val
1 5 10 15

Ser Asn Ile Ser Ser Glu Phe Gly Arg Arg Val Trp Thr Ser Ala Pro
20 25 30

Pro Pro Gln Arg Pro Phe Arg Val Cys Asp His Lys Arg Thr Ile Arg
35 40 45

Lys Gly Leu Thr Ala Ala Thr Arg Gln Glu Leu Leu Ala Lys Ala Leu
50 55 60

Glu Thr Leu Leu Leu Asn Gly Val Leu Thr Leu Val Leu Glu Glu Asp
65 70 75 80

Gly Thr Ala Val Asp Ser Glu Asp Phe Phe Gln Leu Leu Glu Asp Asp
85 90 95

Thr Cys Leu Met Val Leu Gln Ser Gly Gln Ser Trp Ser Pro Thr Arg
100 105 110

Ser Gly Val Leu Ser Tyr Gly Leu Gly Arg Glu Arg Pro Lys His Ser
115 120 125

Lys Asp Ile Ala Arg Phe Thr Phe Asp Val Tyr Lys Gln Asn Pro Arg
130 135 140

Asp Leu Phe Gly Ser Leu Asn Val Lys Ala Thr Phe Tyr Gly Leu Tyr
145 150 155 160

Ser Met Ser Cys Asp Phe Gln Gly Leu Gly Pro Lys Lys Val Leu Arg
165 170 175

Glu Leu Leu Arg Trp Thr Ser Thr Leu Leu Gln Gly Leu Gly His Met
180 185 190

Leu Leu Gly Ile Ser Ser Thr Leu Arg His Ala Val Glu Gly Ala Glu
195 200 205

Gln Trp Gln Gln Lys Gly Arg Leu His Ser Tyr
210 215

<210> 79
 <211> 660
 <212> DNA
 <213> Homo sapiens

<400> 79
 atggagttacc tctcagctct gaaccccaagt gacttactca ggtcagtatc taatataagc 60
 tcggagtttgc acggagggtt ctggaccta gctccaccac cccagcgacc tttccgtgtc 120
 tgtgatcaca agcggaccat ccggaaaggc ctgacagctg ccacccgcca ggagctgcta 180
 gccaaagcat tggagaccct actgctgaat ggagtgcata ccctgggtgct agaggaggat 240
 ggaactgcag tggacagtga ggacttcttc cagctgctgg aggatgacac gtgcctgtatg 300
 gtgttgcagt ctggtcagag ctggagccct acaaggagtg gagtgctgtc atatggcctg 360
 ggacgggaga ggcccaagca cagcaaggac atcgcccgat tcaccttga cgtgtacaag 420
 caaaaaccctc gagacctctt tggcagcctg aatgtcaaag ccacattcta cgggctctac 480
 tctatgagtt gtgactttca aggacttggc ccaaagaaag tactcagggc gtccttcgt 540
 tggacctcca cactgctgca aggctgggc catatgttgc tggaaatttc ctccaccctt 600
 cgtcatgcag tggagggggc tgagcagtgg cagcagaagg gcccctcca ttccctactaa 660

<210> 80
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 80

Gln Val His Leu Ile Gln Ala Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Leu Ser Leu Ile Asn Tyr
 20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
 50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
 65 70 75 80

Lys Met Asn Ser Leu Gln Gly Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Ser Glu Leu Gly Ala Met Asp Tyr Trp Ala Gln Gly Ile Ser
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
130 135 140

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser
145 150 155 160

Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro
165 170 175

Gly Gln Pro Pro Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser
180 185 190

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

Gln His Ile Arg Glu Ala Tyr Thr Phe Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 81
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
gcaatactcc atggccagg tgcattgtat tcaggcgggc ccgggcctgg tgcagccgag 60
ccagagcctg agcattacct gcaccgtgag cggcctgagc ctgattaact atggcgtgca 120
ttgggtgcgt cagagcccg gcaaaggcct ggaatggctg ggctgtgattt ggagccggcgg 180

cageaccgat tataacgcgg cgtttattag ccgtctgagc attagcaaag ataacagcaa	240
aagccaggtg ttttttaaaa tgaacagcct gcagggcaac gataccgcga tttattattg	300
cgcgcgtaac agcgaactgg gcgcgatgga ttattggcg cagggcatta gcgtgaccgt	360
gagcagcggc ggcggcggca gcggcggcgg cggcagcggc ggccggcggca gcgatattgt	420
gctgacccag agcccgccga gcctggcggt gagcctggc cagcgtgcga ccattagctg	480
ccgtgcgagc aaaagcgtga gcaccagcgg ctatagctat atgcattgga accagcagaa	540
accgggccag ccgccgcgtc tgctgattt tctggtgagc aacctggaaa gcggcgtgcc	600
ggcgcgtttt agcggcagcg gcagcggcac cgatttacc ctgaacattc atccggtgga	660
agaagaagat gcggcgacct attattgcca gcatattcgt gaagcgtata cctttggcgg	720
cggcaccaaa ctggaaatta aactcgaggc atagcc	756